

Figure 1A

1	TAGTTCTAGATCGCGAGCGGGCGCCGGCGGGCCGAGGAGGGAGGAAGGAAGGAAGG	60
61	CTGGAAGGAAGGAAGCAGGAAAGAAGAAGGAAAGGAAAGGAAAGGCAAGAAGGAAGG	120
121	GCGGCGGGCGAGGGCGCGGGGCCGGACGGCAGGCGGGCGAGGGCAGGAGGCAGAGCG	180
181	CCCCCCCAGCCCCACCGCCGCCGCTGCCGAAGGCCCCCTCCCCACCCAGGGGCCGGG	240
241	GGGGAGAGCGCGAGAGGGCTCCAGGCCCCGGCAGGCCCCCGCGCCCTCCCCCGCAG	300
301	CGGGCCTTGACCCCCAATTCTGAGCCTCATGGGGGGTCTCCCCCACGGGCCGG	360
361	CATGCTGCCCCCGGAAGGAACCCCTCTCTCGCTCACGATCTCGACAGGAAGCCCTGG	420
421	GAACTGGGAGGCAGAGACCCGGCTGGCGGAGGCATGTGGAGGGGGGCCTGGCGC	480
481	AGGGAGAGGCCAGCGGAAGCCAAGCCACCAGGCCCCCACCGTCCACCGGGAGCATGAA	540
541	CATTGAGGATGGCGCTGCCCCGGCTCCCCGTGCCCCCGCTGCCGCCGGTAGGTGT	600
1	<u>M A R A R G S P C P P L P P G R M S</u>	18
601	CCTGGCCCCACGGGGATTGCTTCCCTGGCTCTCTCCCCACCCCTGGGGCCGGTG	660
19	<u>W P H G A L L F L W L F S P P H G A G G</u>	38
661	GAGGTGGAGTGGCCGTGACCTCTGCCCGGGAGGGGCTCCCCGCCGACACCTCCTGCC	720
39	<u>G G V A V T S A A G G G S P P A T S C P</u>	58
721	CCGTGGCCTGCTCCCTGCAGCAACCAGGCCAGCCGGTGAATCTGCACACGGAGAGACCTGG	780
59	<u>V A C S C S N Q A S R V I C T R R D L A</u>	78
781	CCGAGGTCCCAGCCAGCATCCCGTCAACACGGTACCTGAAACCTGCAAGAGAACGGCA	840
79	<u>E V P A S I P V N T R Y E N H Q E N G I</u>	98
841	TCCAGGTGATCCGGACGGACACGTTAACGCCACCTGCCGACCTGGAGATTCGAGCTGA	900
99	<u>Q V I R T D T F K H L R H L E I H Q H S</u>	118
901	GCAAGAACCTGGTGGCGCAAGATCGAGGTGGCGCCCTCAACGGGCTGCCAGCCTCAACA	960
119	<u>K N L V R K I E V G A F N G H P S H N T</u>	138
961	CGCTGGAGCTTTGACAAACCGGCTGACCGGTGCCACGCAGGCCTTCGAGTACCTGT	1020
139	<u>H E L F D N R L T T V P T Q A F E Y L S</u>	158

Figure 1B

1021	CCAAGCTGCGGGAGCTCTGGCTCGGAAACAACCCCATCGAGAGCATCCCTCCACGCT	1080
159	K W R E I W W R N N P I E S I P S Y A F	178
1081	TCAACCGCGTGCCTCGCTCGGCCGCTGGACCTGGCGAGCTCAAGCGCTGGAATACA	1140
179	N R V P S W R R W D W G E L K R L E Y I	198
1141	TCTCGGAGCGGCCCTCGAGGGCTGGCTAACCTGCGCTACCTAACCTGGGCATGTGCA	1200
199	S E A A F E G L V N L R Y W N N G M C N	218
1201	ACCTCAAGGACATCCCCAACCTGACGGCCCTGGTGCCTCGAGGAGCTGGAGCTGCG	1260
219	L K D I P N L T A L V R W E E L E L S G	238
1261	GCAACCGCTGGACCTGATCCGCCCGGGCTCCTCCAGGTCTCACAGGCTGGCAAGC	1320
239	N R L D L I R P G S F Q G W T S L R K N	258
1321	TGTGGCTCATGCACGCCAGGTAGGCCACATCGAGCGCAACGCCCTCGACGACCTCAAGT	1380
259	W L M H A Q V A T I E R N A F D D L K S	278
1381	CGCTGGAGGAGCTCAACCTGTCCACACAAACCTGATGTCGCTGCCCAAGGACCTCTCA	1440
279	L E E L N L S H N N M S L P H D L F T	298
1441	CGCCCTGCACCGCCTCGAGCGCGTGCACCTCAACCACAACCCCTGGCATTGCAACTGCG	1500
299	P L H R L E R V H L N H N P W H C N C D	318
1501	ACGTGCTCTGGCTGAGCTGGCTCAAGGAGACGGTGCCAGCAACACGACGTGCTGCG	1560
319	V L W L S W W L K E T V P S N T T C C A	338
1561	CCCGCTGTATGCCGCCGCCGCTCAAGGGCGCTACATTGGGAGCTGGACAGTCGC	1620
339	R C H A P A G W K G R Y I G E L D Q S H	358
1621	ATTTCACCTGCTATGCCGCCGTATCGTGAGGCCACGGACCTCAACGTACCGAGG	1680
359	F T C Y A P V I V E F P T D L N V T E G	378
1681	GCATGGCTGCCGAGCTCAAATGCCGCACGGCACCTCCATGACCTCCGTAACCTGGCTGA	1740
379	M A A E L K C R T G T S M T S V N W L T	398
1741	CGCCCAACGGCACCCCATGACCCACGGCTCCACCGCTGGCATTCCGTCTGCATG	1800
399	P N G T L M T H G S Y R V R I S V L H D	418
1801	ACGGCACGCTTAACCTCACCAACGTACCGTCAGGACACGGCCAGTACACGTGCATGG	1860
419	G T L N F T N V T V Q D T G Q Y T C M V	438
1861	TGACGAACCTAGCCGCCAACACCAACCGCCCTGGCACGCTAACGTCTGGCCGTGGACC	1920
439	T N S A G N T T A S A T L N V S A V D P	458

Figure 1C

1921	CCGTGGCGGCCGGGGCACCGGCAGCGCGGGGGCGCCCTGGGGCAGTGGTGGTGGT	1980
459	V A A G G T G S G G G G P G G S G G V G	478
1981	GAGGGGGCAGTGGCGGCCACACCTACTTCACACCAGGTGACCGTGGAGACCTGGAGACGC	2040
479	G G S G G Y T Y F T T V T V E T L E T Q	498
2041	AGCCCGGAGAGGAGGGCCCTGCAGCCGCGGGGACGGAGAAGGAACCGCCAGGGCCCACGA	2100
499	P G E E A L Q P R G T E K E P P G P T T	518
2101	CAGACGGTGTCTGGGTGGGGCCGGCTGGGACGCCGGCCCTGCCTCGTCTTCTA	2160
519	D G V W G G G R P G D A A G P A S S S T	538
2161	CCACGGCACCCGGCCCGCCTCTCGCGGCCACGGAGAAGCGTTACCGGTGCCATCA	2220
539	T A P A P R S S R P T E K A F T V P I T	558
2221	CGGATGTGACGGAGAACGCCCTCAAGGACCTGGACGACGTCAAGAACCAAAATCA	2280
559	D V T E N A L K D L D D V M K T T K I I	578
2281	TCATCGGCTGCTTGTGGCCATCACGTTATGGCCGCGGTGATGCTCGTGGCCTCTACA	2340
579	I G C F V A I T F M A A V M L V A F Y K	598
2341	AGCTGCGCAAGCAGCACCAAGCTCCACAAGCACCAACGGGCCACGCGCACCGTGGAGATCA	2400
599	L R K Q H Q L H K H H G P T R T V E I I	618
2401	TCAACGTGGAGGGACGAGCTGCCGCCCTCGGCCGTGTCGTGGCCGCC	2450
619	N V E D E L P A A S A V S V A A	634

10028392001

Figure 2A

Figure 2B

HLRRNS-1
 KIAA1580
 BOVIN_CHONDROADHERIN_PRECURSOR
 SLIT-2.

 HLRRNS-1
 KIAA1580
 BOVIN_CHONDROADHERIN_PRECURSOR
 SLIT-2.

 HLRRNS-1
 KIAA1580
 BOVIN_CHONDROADHERIN_PRECURSOR
 SLIT-2.

 HLRRNS-1
 KIAA1580
 BOVIN_CHONDROADHERIN_PRECURSOR
 SLIT-2.

 HLRRNS-1
 KIAA1580
 BOVIN_CHONDROADHERIN_PRECURSOR
 SLIT-2.

QDTGQTCMVNTNSAGNTTASATLNVSADVPAAGGTGSGGGPGGSGGVG
 QDTGMITCMVSNVGNNTTASATLNVT-----AT-----TT
 EATGIFKKLQLRKINLSNNKITDIEEGAFEGASG-----VN
 :
 GGSGGTTTIVTVELETQPGEEALQPRGTEKEPPGPTTDGVGGGPG
 P---FSYFSTVTVETMEPSQOE---ARTDNNN-VGPTPVVDW---
 EILLTSNRLENVQHMKFKGLESLTKLMLRSNRISCVG-ND5FTGLGSVR
 :
 DAAGPASSSTTAPAPRSSRPTEAKFTVPIDVTE-ALKLDLDDVMFTTKI
 -----ETNVITSLTFQSTRSTETFTIPVTDINS--GIPGIDEVMMTTKI
 -----LSLYDNQITTVAPGAFGTLHSLSTLNLLANPFNCNCHLAWLGEWLRKKI
 :
 IIG---CFVAITFMAAVMLVAFYKLRRQHQLHKKHGPTRTVEIINVEDEL
 IIG---CFVAITLMAAVMLVIFYKMRKQHHRQNHAPTRTVIEINVDDEI
 -----VTGNPRCOKFYFLKEIPQDQVIAQDFTCDDGNDNSCPLSRCPSETCL
 :
 PAASAVSVAA-----
 TGDTPMESHLPMPAIEHEHLHNHYNSYKSPFNHTTTVNTINSIHSSVHEPL
 -----DTVVRCNSNKGKVLPKGIPRDVTEYLQDNQFTLVPEFFFFFFFLSIF
 :
 LIRMNNSKDNVQETQI-

 FLFETGSGGVASALEY

10028392-122001

Figure 3

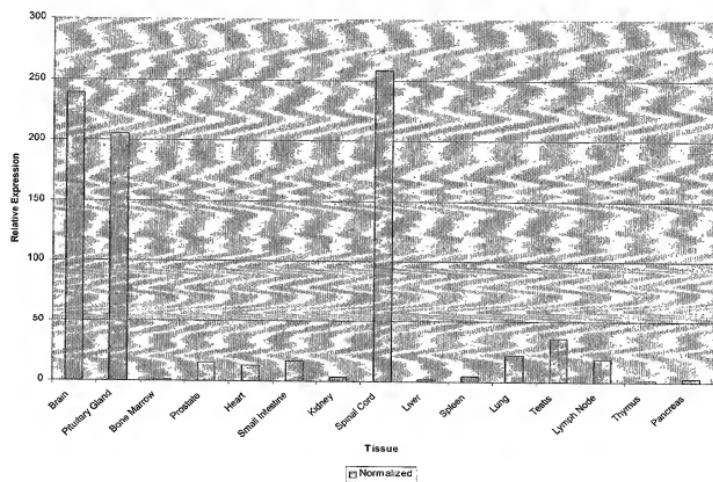


Figure 5B

Figure 4A

1	CCACCGTCCGACTAGTTCTAGATCGCGAGCGCGCGCGCGGGGCCGAGGAGGGAGGAAG	60
61	GAAGGAAGGAAGGCTGAGGAAGGAAGCCAGGAAGAAAGAAGGAAGGAAGGAAGGCA	120
121	AGAAGGAAGGCAGGGCGGGCGGGCGAGGGCGCGGGGCCGAGGGCAGGGCGCGAGGC	180
181	GGAGGCAGAGCGGCCCCCCCAGCCCCACCGCCCGCCTCGCGAAGCCCCCTCCCCACCC	240
241	GGAGCCGGGGAGGGGGAGAGCGCGAGAGGCTCCAGGCCGGCCGAGCCCCGGGG	300
301	CGCCTCCCCGAGCGGGCCTTGACCCCCAATTCTGAGCCTCATGGGGGGTCCTCCCC	360
361	CCCACGGCCGGCATGCTGCCCGGAGGAAGGAACCCCTCTCTCGCTCACGATCTCGAC	420
421	AGGAAGCCCTGGAGAACTGGGGAGGCAGAGACCCCGCTGGCCGGAGGCATGTGGAGGG	480
481	GGGGCCTGGCGCAGGGAGAGGCCAGCGGAAGCCAAGCCACCAGGCCCGTCC	540
541	CGCGGAGCATGAACATTGAGGATGGCGCGTGCCTCGGGCTCCCCGTGCCCGCTGCCG	600
1	M A R A R G S P C P P L P	13
601	CCCGGTAGGATGTCCTGGCCCCACGGGCATTGCTCTTCTCTGGCTCTCTCCCCACCC	660
14	P G R M S W F H G A L L F L W L F S P P	33
661	CTGGGGCCGGTGGAGGTGGAGTGGCCGTGACGTCTGCCCGGAGGGGGCTCCCCCG	720
34	<u>M G A</u> G G G G V A V T S A A G G G G S P P	53
721	GCCACCTCTGCCCGTGGCTGCTCTGCAGCAACCAGGCCAGCCGGTGTCTGCACA	780
54	A T S C P V A C S C S N Q A S R V I C T	73
781	CGGAGAGACCTGGCGAGGTCCAGCCAGCATCCGGTCAACACGCCGTTAACCTGAAACCTG	840
74	R R D E A E V P A S I P V N T R Y L N	93
841	CAAGAGAACGGCATCCAGGTGATCCGGACGGACAGTTCAAGCACCTGGGGCACCTGGAG	900
94	Q E N G I Q V I R T D T F K H L R H L E	113
901	ATTCTGCAGCTGGAGCAAGAACCTGGTGGCGCAAGATCGAGGTGGCCCTTCAACGGCTG	960
114	I <u>Q</u> L S K N L V R K I E V G A F N G L	133
961	CCAGCCTAACACGCTGGAGCTTTTGACAACCGGCTGACCACGGTGCCACGCAGGCC	1020
134	P S L N T <u>E</u> F D N R L T T V P T Q A	153

Figure 4B

1021	TTCGAGTACCTGTCCAAGCTGGGGAGCTCTGGCTGCGGAACAAACCCATCGAGAGCATC	1080
154	F E Y L S K R E L W D R N N P I E S I	173
1081	CCCTCCTACGCCCTCAACCGCGTGCCTCGCTGCGCGCCCTGGACCTGGCGAGCTCAAG	1140
174	P S Y A F N R V P S R R D E G E L K	193
1141	CGGCTGGAATACATCTGGAGGGCGCCCTCGAGGGGCTGGTCAACCTGCCCTACCTCAAC	1200
194	R L E Y I S E A A F E G L V N R Y N	213
1201	CTGGGCATGTGCAACCTCAAGGACATCCCAACCTGACGGCCCTGGTGCCTGGAGGAG	1260
214	Q G M C N L K D I P N L T A L V R E E	233
1261	CTGGAGCTGTGGGCAACCGGCTGGACCTGATCGGCCCGGGCTCCTCCAGGGTCTCAC	1320
234	Q E L S G N R L D L I R P G S F Q G L T	253
1321	AGCCTGCGAAGCTGTGGCTCATGCACGCCAGGTAGCCACCATCGAGCGCAACGCCCTC	1380
254	S L R K R W L M H A Q V A T I E R N A F	273
1381	GACGACCTCAAGTCGCTGGAGGAGCTCAACCTGTCCCAACACACCTGATTCGCTGCC	1440
274	D D L K S L E E L N L S H N N M S L P	293
1441	CACGACCTCTCACGCCCTGACCCGCTCGAGCGCTGACCTCAACACAAACCCCTGG	1500
294	H D L F T P L H R L E R V H N H N P W	313
1501	CATTGCAACTGCGACGTGCTGGCTGAGCTGGCTCAAGGAGACGGTGCAGCAAC	1560
314	H C N C D V L W L S W W L K E T V P S N	333
1561	ACGACGTGCTGCCCGCTGTCATGCCCGCCGCCCTCAAGGGGCTACATTGGGAG	1620
334	T T C C A R C H A P A G R Y I G E	353
1621	CTGGACCATGCGATTCAACCTGCTATGGCCCGCTCATCGTGGCTGAGCCGCCACGGACCTC	1680
354	L D Q S H F T C Y A P V I V E P P T D L	373
1681	AACGTACCGAGGGCATGGCTGCCGAGCTCAAATGCCGACGGCACCTCCATGACCTCC	1740
374	N V T E G M A A E L K C R T G T S M T S	393
1741	GTCACACTGGCTGACGCCAACGGCACCTCATGACCCACGGCTCTACCGCGTGCAC	1800
394	V N W L T P N G T L M T H G S Y R V R I	413
1801	TCCGTCTGCATGACGGCACGCTTAACCTCACCAACGTCACCGTGCAGGACACGGCCAG	1860
414	S V L H D G T L N F T N V T V Q D T G Q	433
1861	TACACGTGATGGTGACGAACCTAGCCGGCAACACCACCGCCTGGCCACGCTCAACGTC	1920
434	Y T C M V T N S A G N T T A S A T L N V	453

100028392-1882

Figure 4C

1921	TCGGCCGTGGACCCCGTGGCGGCCGGGGCACCGGCAGCGGCCGGGGCGGCCCTGGGGC	1980
454	S A V D P V A A G G T G S G G G P G G	473
1981	AGTGGTGGTGTGGAGGGGGCAGTGGCGCTACACCTACITCACCACGGTGACCGTGGAG	2040
474	S G G V G G G S G G Y T Y F T T V T V E	493
2041	ACCCCTGGAGACGCAGCCCGGAGAGGAGGCCCTGCAGCCCGGGGGACGGAGAAGGAACCG	2100
494	T L E T Q P G E E A L Q P R G T E K E P	513
2101	CCAGGGCCCACGACAGACGGTGTCTGGGGTGGGGCCGGCTGGGGACGGCCGGCCCT	2160
514	P G P T T D G V W G G G R P G D A A G P	533
2161	GCCTCGTCTTACACCGCACCCGCCCGCGCTCTCGGGCCACGGAGAAGGCCTTC	2220
534	A S S S T T A P A P R S S R P T E K A F	553
2221	ACGGTGCCCCATCACGGATGTGACGGAGAACGCCCTAACGGACCTGGACGACGTATGAAG	2280
554	T V P I T D V T E N A L K D L D D V M K	573
2281	ACCAACAAAATCATCATCGCGTCTCGGTGGCCATCACGTTCTGGCGCGGTGATGTC	2340
574	T T K I I I G C F V A I T F M A A V M L	593
2341	GTGGCCTTCTACAAGCTGCGCAAGCAGCACCGAGCTCCACAAAGCACACGGGCCACGC	2400
594	V A F Y K L R K Q H Q L H K H H G P T R	613
2401	ACCGTGGAGATCATCAACGTGGAGGACGAGCTGCCGCCGCTCGGCCGTGTCCGTGGCC	2460
614	T V E I I N V E D E L P A A S A V S V A	633
2461	GCCGCCGCCGCGCTGGCCAGTGGGGTGGTGTGGCGGGGACAGCCACCTGGCCCTGCC	2520
634	A A A A V A S G G G V G G D S H L A L P	653
2521	GCCCTGGAGCAGACCACTCAACCCACCAACTACGTGGCTGCCGCCCTCAAGGCGCAC	2580
654	A L E R D H L N H H H Y V A A A A F K A H	673
2581	TACAGCAGCAACCCACGGCGGGGCTCGGGGGCAAAAGGCCGCCCTGGCCTCAACTCC	2640
674	Y S S N P S G G G C G G K G P P G L N S	693
2641	ATCCACGAACCTCTGCTCTTCAGAGCCGGTCCAAGGAGAACGTGCAAGAGACCCAGATC	2700
694	I H E P L L F K S G S K E N V Q E T Q I	713
2701	TGAGGGCGGGCGGGCGGGCGGGCGAGGGCGTGGAGCCCCCACCGGTCCCAGC	2756

10028392-122061

Figure 6.

HLRRSI1 (SEQ ID NO:2)

Protein	Genbank ID	Identities	Similarities
bovine chondroadherin precursor	gi 627724	32.3%	37.4%
rat slit-2	gi 6579191	26.7%	33.8%
KIAA1580	gi 10047235	73.9%	65.5%

HLRRSI1 (SEQ ID NO:35)

Protein	Genbank ID	Identities	Similarities
bovine chondroadherin precursor	gi 627724	32.3%	37.4%
rat slit-2	gi 6579191	26.7%	33.8%
KIAA1580	gi 10047235	68.0%	75.5%